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TECH



1600

RAW SEQUENCE LISTING

DATE: 08/28/2003

PATENT APPLICATION: US/09/830,026B

TIME: 10:39:12

Input Set : A:\UOK532.ST25.txt

Output Set: N:\CRF4\08282003\I830026B.raw

3 <110> APPLICANT: University of Kansas Center for Research
 4 Walter Reed Army Institute for Research
 6 <120> TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF PURIFIED INVASIN PROTEIN AND
 USE THEREOF

8 <130> FILE REFERENCE: UOK 5320.1

C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/830,026B

C--> 11 <141> CURRENT FILING DATE: 2001-10-20

13 <150> PRIOR APPLICATION NUMBER: PCT/US99/24931

14 <151> PRIOR FILING DATE: 1999-10-21

16 <160> NUMBER OF SEQ ID NOS: 18

18 <170> SOFTWARE: PatentIn version 3.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 409

22 <212> TYPE: PRT

23 <213> ORGANISM: Salmonella typhimurium

25 <400> SEQUENCE: 1

27 Met Leu Ile Ser Asn Val Gly Ile Asn Pro Ala Ala Tyr Leu Asn Asn

28 1 5 10 15

31 His Ser Val Glu Asn Ser Ser Gln Thr Ala Ser Gln Ser Val Ser Ala

32 20 25 30

35 Lys Asp Ile Leu Asn Ser Ile Gly Ile Ser Ser Ser Lys Val Ser Asp

36 35 40 45

39 Leu Gly Leu Ser Pro Thr Leu Ser Ala Pro Ala Pro Gly Val Leu Thr

40 50 55 60

43 Gln Thr Pro Gly Thr Ile Thr Ser Ser Leu Lys Ala Ser Ile Gln Asn

44 65 70 75 80

47 Thr Asp Met Asn Gln Asp Leu Asn Ala Leu Ala Asn Asn Val Thr Thr

48 85 90 95

51 Lys Ala Asn Glu Val Val Gln Thr Gln Leu Arg Glu Gln Gln Ala Glu

52 100 105 110

55 Val Gly Lys Phe Phe Asp Ile Ser Gly Met Ser Ser Ser Ala Val Ala

56 115 120 125

59 Leu Leu Ala Ala Ala Asn Thr Leu Met Leu Thr Leu Asn Gln Ala Asp

60 130 135 140

63 Ser Lys Leu Ser Gly Lys Leu Ser Leu Val Ser Phe Asp Ala Ala Lys

64 145 150 155 160

67 Thr Thr Ala Ser Ser Met Met Arg Glu Gly Met Asn Ala Leu Ser Gly

68 165 170 175

71 Ser Ile Ser Gln Ser Ala Leu Gln Leu Gly Ile Thr Gly Val Gly Ala

72 180 185 190

75 Lys Leu Glu Tyr Lys Gly Leu Gln Asn Glu Arg Gly Ala Leu Lys His

76 195 200 205

79 Asn Ala Ala Lys Ile Asp Lys Leu Thr Thr Glu Ser His Ser Ile Lys

80 210 215 220

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83 Asn Val Leu Asn Gly Gln Asn Ser Val Lys Leu Gly Ala Glu Gly Val
84 225          230          235          240
87 Asp Ser Leu Lys Ser Leu Asn Ile Arg Lys Pro Val Pro Met Arg Arg
88          245          250          255
91 Lys Ile Leu Met Met Arg Arg Leu Asn Leu Met Pro Glu Pro Ala Pro
92          260          265          270
95 Arg Lys Val Trp Val Leu Lys Thr Val Ile Asn Lys Val Ser Leu Asn
96          275          280          285
99 Ile Tyr Ile Leu Ser Lys Arg Leu Glu Ser Val Glu Ser Asp Ile Arg
100          290          295          300
103 Leu Glu Gln Asn Tyr Met Asp Ile Thr Arg Ile Asp Ser Ala Gln Asp
104 305          310          315          320
107 Ala Asp Asp Gly Arg Ser Asp Tyr Glu Glu Leu Gly His Gly Arg Trp
108          325          330          335
111 Tyr Cys Arg Gly Val Arg Ala Val Arg Arg Tyr Ser Gly Asn Val Ser
112          340          345          350
115 Glu Gln Gln Ile Ser Gln Val Asn Asn Arg Val Ala Ser Thr Ala Ser
116          355          360          365
119 Asp Glu Ala Arg Glu Ser Ser Arg Lys Ser Thr Ser Leu Ile Gln Glu
120          370          375          380
123 Met Leu Lys Thr Met Glu Ser Ile Asn Gln Ser Lys Ala Ser Ala Leu
124 385          390          395          400
127 Ala Ala Ile Ala Gly Asn Ile Arg Ala
128          405
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 382
133 <212> TYPE: PRT
134 <213> ORGANISM: Shigella flexneri
136 <400> SEQUENCE: 2
138 Met Leu Gln Lys Gln Phe Cys Asn Lys Leu Leu Leu Asp Thr Asn Lys
139 1          5          10          15
142 Glu Asn Val Met Glu Ile Gln Asn Thr Lys Pro Thr Gln Thr Leu Tyr
143          20          25          30
146 Thr Asp Ile Ser Thr Lys Gln Thr Gln Ser Ser Ser Glu Thr Gln Lys
147          35          40          45
150 Ser Gln Asn Tyr Gln Gln Ile Ala Ala His Ile Pro Leu Asn Val Gly
151          50          55          60
154 Lys Asn Pro Val Leu Thr Thr Thr Leu Asn Asp Asp Gln Leu Leu Lys
155 65          70          75          80
158 Leu Ser Glu Gln Val Gln His Asp Ser Glu Ile Ile Ala Arg Leu Thr
159          85          90          95
162 Asp Lys Lys Met Lys Asp Leu Ser Glu Met Ser His Thr Leu Thr Pro
163          100          105          110
166 Glu Asn Thr Leu Asp Ile Ser Ser Leu Ser Ser Asn Ala Val Ser Leu
167          115          120          125
170 Ile Ile Ser Val Ala Val Leu Leu Ser Ala Leu Arg Thr Ala Glu Thr
171          130          135          140
174 Lys Leu Gly Ser Gln Leu Ser Leu Ile Ala Phe Asp Ala Thr Lys Ser
175 145          150          155          160

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178 Ala Ala Glu Asn Ile Val Arg Gln Gly Leu Ala Ala Leu Ser Ser Ser
179                               165                               170                               175
182 Ile Thr Gly Ala Val Thr Gln Val Gly Ile Thr Gly Ile Gly Ala Lys
183                               180                               185                               190
186 Lys Thr His Ser Gly Ile Ser Asp Gln Lys Gly Ala Leu Arg Lys Asn
187                               195                               200                               205
190 Leu Ala Thr Ala Gln Ser Leu Glu Lys Glu Leu Ala Gly Ser Lys Leu
191                               210                               215                               220
194 Gly Leu Asn Lys Gln Ile Asp Thr Asn Ile Thr Ser Pro Gln Thr Asn
195 225                               230                               235                               240
198 Ser Ser Thr Lys Phe Leu Gly Lys Asn Lys Leu Ala Pro Asp Asn Ile
199                               245                               250                               255
202 Ser Leu Ser Thr Glu His Lys Thr Ser Leu Ser Ser Pro Asp Ile Ser
203                               260                               265                               270
206 Leu Gln Asp Lys Ile Asp Thr Gln Arg Arg Thr Tyr Glu Leu Asn Thr
207                               275                               280                               285
210 Leu Ser Ala Gln Gln Lys Gln Asn Ile Gly Arg Ala Thr Met Glu Thr
211                               290                               295                               300
214 Ser Ala Val Ala Gly Asn Ile Ser Thr Ser Gly Gly Arg Tyr Ala Ser
215 305                               310                               315                               320
218 Ala Leu Glu Glu Glu Glu Gln Leu Ile Ser Gln Ala Ser Ser Lys Gln
219                               325                               330                               335
222 Ala Glu Glu Ala Ser Gln Val Ser Lys Glu Ala Ser Gln Ala Thr Asn
223                               340                               345                               350
226 Gln Leu Ile Gln Lys Leu Leu Asn Ile Ile Asp Ser Ile Asn Gln Ser
227                               355                               360                               365
230 Lys Asn Ser Ala Ala Ser Gln Ile Ala Gly Asn Ile Arg Ala
231                               370                               375                               380
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 4
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: NdeI restriction site
242 <400> SEQUENCE: 3
243 gaga
246 <210> SEQ ID NO: 4
247 <211> LENGTH: 29
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: PCR Primer
254 <400> SEQUENCE: 4
255 gagacatatg ttatcagagc aggttcagc
258 <210> SEQ ID NO: 5
259 <211> LENGTH: 30
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:

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264 <223> OTHER INFORMATION: PCR Primer
266 <400> SEQUENCE: 5
267 gagaggatcc ttaagctcga atgttaccag 30
270 <210> SEQ ID NO: 6
271 <211> LENGTH: 27
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: PCR Primer
278 <400> SEQUENCE: 6
279 gagacatatg ttgcaaaagc aatttgc 27
282 <210> SEQ ID NO: 7
283 <211> LENGTH: 32
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: PCR Primer
290 <400> SEQUENCE: 7
291 gagaggatcc ttaggtgtca attttatcct gc 32
294 <210> SEQ ID NO: 8
295 <211> LENGTH: 29
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: PCR Primer
302 <400> SEQUENCE: 8
303 gagacatatg ttatcagagc aggttcagc 29
306 <210> SEQ ID NO: 9
307 <211> LENGTH: 32
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: PCR Primer
314 <400> SEQUENCE: 9
315 gagaggatcc ttaggtgtca attttatcct gc 32
318 <210> SEQ ID NO: 10
319 <211> LENGTH: 22
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: PCR Primer
326 <400> SEQUENCE: 10
327 gagacatatg ttgcaaaagc aa 22
330 <210> SEQ ID NO: 11
331 <211> LENGTH: 29
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: PCR Primer

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338 <400> SEQUENCE: 11
339 gagactcgag atgcgttttt ttggcaccg 29
342 <210> SEQ ID NO: 12
343 <211> LENGTH: 29
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
348 <223> OTHER INFORMATION: PCR Primer
350 <400> SEQUENCE: 12
351 gagactcgag acccagagaa gaacttacg 29
354 <210> SEQ ID NO: 13
355 <211> LENGTH: 30
356 <212> TYPE: DNA
357 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: PCR Primer
362 <400> SEQUENCE: 13
363 gagaggatcc ttaagctcga atgttaccag 30
366 <210> SEQ ID NO: 14
367 <211> LENGTH: 27
368 <212> TYPE: DNA
369 <213> ORGANISM: Artificial Sequence
371 <220> FEATURE:
372 <223> OTHER INFORMATION: PCR Primer
374 <400> SEQUENCE: 14
375 gagacatatg ttgcaaaaagc aatttgc 27
378 <210> SEQ ID NO: 15
379 <211> LENGTH: 31
380 <212> TYPE: DNA
381 <213> ORGANISM: Artificial Sequence
383 <220> FEATURE:
384 <223> OTHER INFORMATION: PCR Primer
386 <400> SEQUENCE: 15
387 gagactcgag taactttaaa agttgatcat c 31
390 <210> SEQ ID NO: 16
391 <211> LENGTH: 28
392 <212> TYPE: DNA
393 <213> ORGANISM: Artificial Sequence
395 <220> FEATURE:
396 <223> OTHER INFORMATION: PCR Primer
398 <400> SEQUENCE: 16
399 gagactcgag cttgccactg ctcaatct 28
402 <210> SEQ ID NO: 17
403 <211> LENGTH: 30
404 <212> TYPE: DNA
405 <213> ORGANISM: Artificial Sequence
407 <220> FEATURE:
408 <223> OTHER INFORMATION: PCR Primer
410 <400> SEQUENCE: 17

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date